



20093A-21US-Substitute Sequence Listing.txt
SEQUENCE LISTING

<110> Murphy, Gerald P.
Boynton, Alton L.
Sehgal, Anil

<120> Nr-CAM GENE, NUCLEIC ACIDS AND NUCLEIC ACID PRODUCTS
FOR THERAPEUTIC AND DIAGNOSTIC USES FOR TUMORS

<130> 20093A-002100US

<140> 09/301,380
<141> 1999-04-27

<150> 60/112,098
<151> 1998-12-14

<150> 60/083,152
<151> 1998-04-27

<160> 33

<170> PatentIn Ver. 2.0

<210> 1
<211> 4134
<212> DNA
<213> Homo sapiens

<220>
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cttaaaaata atg ccg aaa aag aag cgc tta tct gcg ggc aga gtg ccc ctg 171
Met Pro Lys Lys Lys Arg Leu Ser Ala Gly Arg Val Pro Leu
1 5 10

att ctc ttc ctg tgc cag atg att agt gca ctg gaa gta cct ctt gat 219
Ile Leu Phe Leu Cys Gln Met Ile Ser Ala Leu Glu Val Pro Leu Asp
15 20 25 30

cca aaa ctt ctt gaa gac ttg gta cag cct cca acc atc acc caa cag 267
Pro Lys Leu Leu Glu Asp Leu Val Gln Pro Pro Thr Ile Thr Gln Gln
35 40 45

tct cca aaa gat tac att att gac cct cgg gag aat att gta atc cag 315
Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile Val Ile Gln
50 55 60

tgt gaa gcc aaa ggg aaa ccg ccc cca agc ttt tcc tgg acc cgt aat 363
Cys Glu Ala Lys Gly Lys Pro Pro Ser Phe Ser Trp Thr Arg Asn
65 70 75

ggg act cat ttt gac atc gat aaa gac cct ctg gtc acc atg aag cct 411
Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr Met Lys Pro
80 85 90

ggc aca gga acg ctc ata att aac atc atg agc gaa ggg aaa gct gag 459
Gly Thr Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly Lys Ala Glu
95 100 105 110

acc tat gaa gga gtc tat cag tgt aca gca agg aac gaa cgc gga gct 507

20093A-21US-Substitute Sequence Listing.txt

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Ala	Val	Ser	Asn	Asn	Ile	Val	Val	Arg	Pro	Ser	Arg	Ser	Pro	Leu	Trp	
130					135									140		
acc	aaa	gaa	aaa	ctt	gaa	cca	atc	aca	ctt	caa	agt	ggt	cag	tct	tta	603
Thr	Lys	Glu	Lys	Leu	Glu	Pro	Ile	Thr	Leu	Gln	Ser	Gly	Gln	Ser	Leu	
145					150					155						
gta	ctt	ccc	tgc	aga	ccc	cca	att	gga	tta	cca	cca	cct	ata	ata	ttt	651
Val	Leu	Pro	Cys	Arg	Pro	Pro	Ile	Gly	Leu	Pro	Pro	Pro	Ile	Ile	Phe	
160					165					170						
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Trp	Met	Asp	Asn	Ser	Phe	Gln	Arg	Leu	Pro	Gln	Ser	Glu	Arg	Val	Ser	
175					180					185					190	
caa	ggg	ttg	aat	ggg	gac	ctt	tat	ttt	tcc	aat	gtc	ctc	cca	gag	gac	747
Gln	Gly	Leu	Asn	Gly	Asp	Leu	Tyr	Phe	Ser	Asn	Val	Leu	Pro	Glu	Asp	
195					200					205						
acc	cgc	gaa	gac	tat	atc	tgt	tat	gct	aga	ttt	aat	cat	act	caa	acc	795
Thr	Arg	Glu	Asp	Tyr	Ile	Cys	Tyr	Ala	Arg	Phe	Asn	His	Thr	Gln	Thr	
210					215					220						
ata	cag	cag	aag	caa	cct	att	tct	gtg	aag	gtg	att	tca	gtg	gat	gaa	843
Ile	Gln	Gln	Lys	Gln	Pro	Ile	Ser	Val	Lys	Val	Ile	Ser	Val	Asp	Glu	
225					230					235						
ttg	aat	gac	act	ata	gct	gct	aat	ttg	agt	gac	act	gag	ttt	tat	ggt	891
Leu	Asn	Asp	Thr	Ile	Ala	Ala	Asn	Leu	Ser	Asp	Thr	Glu	Phe	Tyr	Gly	
240					245					250						
gct	aaa	tca	agt	aga	gag	agg	cca	cca	aca	ttt	tta	act	cca	gaa	ggc	939
Ala	Lys	Ser	Ser	Arg	Glu	Arg	Pro	Pro	Thr	Phe	Leu	Thr	Pro	Glu	Gly	
255					260					265					270	
aat	gca	agt	aac	aaa	gag	gaa	tta	aga	gga	aat	gtg	ctt	tca	ctg	gag	987
Asn	Ala	Ser	Asn	Lys	Glu	Glu	Leu	Arg	Gly	Asn	Val	Leu	Ser	Leu	Glu	
275					280					285						
tgc	att	gca	gaa	gga	ctg	cct	acc	cca	att	att	tac	tgg	gca	aag	gaa	1035
Cys	Ile	Ala	Glu	Gly	Leu	Pro	Thr	Pro	Ile	Ile	Tyr	Trp	Ala	Lys	Glu	
290					295					300						
gat	gga	atg	cta	ccc	aaa	aac	agg	aca	gtt	tat	aag	aac	ttt	gag	aaa	1083
Asp	Gly	Met	Leu	Pro	Lys	Asn	Arg	Thr	Val	Tyr	Lys	Asn	Phe	Glu	Lys	
305					310					315						
acc	ttg	cag	atc	att	cat	gtt	tca	gaa	gca	gac	tct	gga	aat	tac	caa	1131
Thr	Leu	Gln	Ile	Ile	His	Val	Ser	Glu	Ala	Asp	Ser	Gly	Asn	Tyr	Gln	
320					325					330						
tgt	ata	gca	aaa	aat	gca	tta	gga	gcc	atc	cac	cat	acc	att	tct	gtt	1179
Cys	Ile	Ala	Lys	Asn	Ala	Leu	Gly	Ala	Ile	His	His	Thr	Ile	Ser	Val	
335					340					345					350	
aga	gtt	aaa	gca	gct	cca	tac	tgg	atc	aca	gcc	cct	caa	aat	ctt	gtg	1227
Arg	Val	Lys	Ala	Ala	Pro	Tyr	Trp	Ile	Thr	Ala	Pro	Gln	Asn	Leu	Val	
355					360					365						
ctg	tcc	cca	gga	gag	gat	ggg	acc	ttg	atc	tgc	aga	gct	aat	gac	aac	1275
Leu	Ser	Pro	Gly	Glu	Asp	Gly	Thr	Leu	Ile	Cys	Arg	Ala	Asn	Gly	Asn	
370					375					380						

20093A-21US-Substitute Sequence Listing.txt

ccc aaa ccc aga att agc tgg tta aca aat gga gtc cca ata gaa att	385	390	395	1323
Pro Lys Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile				
gcc cct gat gac ccc agc aga aaa ata gat ggc gat acc att att ttt	400	405	410	1371
Ala Pro Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr Ile Ile Phe				
tca aat gtt caa gaa aga tca agt gca gta tat cag tgc aat gcc tct	415	420	425	1419
Ser Asn Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser				
aat gaa tat gga tat tta ctg gca aac gca ttt gta aat gtg ctg gct	435	440	445	1467
Asn Glu Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala				
gag cca cca cga atc ctc aca cct gca aac aca ctc tac cag gtc att	450	455	460	1515
Glu Pro Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile				
gca aac agg cct gct tta cta gac tgt gcc ttc ttt ggg tct cct ctc	465	470	475	1563
Ala Asn Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu				
cca acc atc gag tgg ttt aaa gga gct aaa gga agt gct ctt cat gaa	480	485	490	1611
Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu				
gat att tat gtt tta cat gaa aat gga act ttg gaa atc aaa gat gct	495	500	505	1659
Asp Ile Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala				
aca tgg atc gtt aaa gaa att cct gtg gcc caa aag gac agt aca gga	515	520	525	1707
Thr Trp Ile Val Lys Glu Ile Pro Val Ala Gln Lys Asp Ser Thr Gly				
act tat acg tgt gtt gca agg aat aaa tta ggg atg gca aag aat gaa	530	535	540	1755
Thr Tyr Thr Cys Val Ala Arg Asn Lys Leu Gly Met Ala Lys Asn Glu				
gtt cac tta cag ccc gaa tat gca gtt gtg caa aga ggg agc atg gtg	545	550	555	1803
Val His Leu Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val				
tcc ttt gaa tgc aaa gtg aaa cat gat cac acc tta tcc ctc act gtc	560	565	570	1851
Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val				
ctg tgg ctg aag gac aac agg gaa ctg ccc agt gat gaa agg ttc act	575	580	585	1899
Leu Trp Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr				
gtt gac aag gat cat cta gtg gta gct gat gtc agt gac gat gac agc	595	600	605	1947
Val Asp Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser				
ggg acc tac acg tgt gtg gcc aac acc act ctg gac agc gtc tcc gcc	610	615	620	1995
Gly Thr Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala				
agc gct gtg ctt agc gtt gtt gct cct act cca act cca gct ccc gtt	625	630	635	2043
Ser Ala Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val				
tac gat gtc cca aat cct ccc ttt gac tta gaa ctg aca gat caa ctt	640	645	650	2091
Tyr Asp Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu				

20093A-21US-Substitute Sequence Listing.txt

gac aaa agt gtt cag ctg tca tgg acc cca ggc gat gac aac aat agc	2139
Asp Lys Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser	
655 660 665 670	
ccc att aca aaa ttc atc atc gaa tat gaa gat gca atg cac aag cca	2187
Pro Ile Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro	
675 680 685	
ggg ctg tgg cac cac caa act gaa gtt tct gga aca cag acc aca gcc	2235
Gly Leu Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala	
690 695 700	
cag ctg aag ctg tct cct tac gtg aac tac tcc ttc cgc gtg atg gca	2283
Gln Leu Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala	
705 710 715	
gtg aac agc att ggg aag agc ttg ccc agc gag gcg tct gag cag tat	2331
Val Asn Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr	
720 725 730	
ttg acg aaa gcc tca gaa cca gat aaa aac ccc aca gct gtg gaa gga	2379
Leu Thr Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly	
735 740 745 750	
ctg gga tca gag cct gat aat ttg gag att acg tgg aag ccc ttg aat	2427
Leu Gly Ser Glu Pro Asp Asn Leu Glu Ile Thr Trp Lys Pro Leu Asn	
755 760 765	
ggt ttc gaa tct aat ggg cca ggc ctt cag tac aaa gtt agc tgg cgc	2475
Gly Phe Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg	
770 775 780	
cag aaa gat ggt gat gat gaa tgg aca tct gtg gtt gtg gca aat gta	2523
Gln Lys Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val	
785 790 795	
tcc aaa tat att gtc tca ggc acg cca acc ttt gtt cca tac ctg atc	2571
Ser Lys Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile	
800 805 810	
aaa gtt cag gcc ctg aat gac atg ggg ttt gcc ccc gag cca gct gta	2619
Lys Val Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val	
815 820 825 830	
gtc atg gga cat tct gga gaa gac ctc cca atg gtg gct cct ggg aac	2667
Val Met Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn	
835 840 845	
gtg cgt gtg aat gtg gtg aac agt acc tta gcc gag gtg cac tgg gac	2715
Val Arg Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp	
850 855 860	
cca gta cct ctg aaa agc atc cga gga cac cta caa ggc tat cgg att	2763
Pro Val Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile	
865 870 875	
tac tat tgg aag acc cag agt tca tct aaa aga aac aga cgt cac att	2811
Tyr Tyr Trp Lys Thr Gln Ser Ser Lys Arg Asn Arg Arg His Ile	
880 885 890	
gag aaa aag atc ctc acc ttc caa ggc agc aag act cat ggc atg ttg	2859
Glu Lys Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu	
895 900 905 910	
ccg ggg cta gag ccc ttt agc cac tac aca ctg aat gtc cga gtg gtc	2907
Pro Gly Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val	

20093A-21US-Substitute Sequence Listing.txt

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cca gaa gga gtc ccc agt gct ccc tcg tct ttg aag att gtg aat cca Pro Glu Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro 945 950 955		3003
aca ctg gac tct ctc act ttg gaa tgg gat cca ccg agc cac ccg aat Thr Leu Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn 960 965 970		3051
ggc att ttg aca gag tac acc tta aag tat cag cca att aac agc aca Gly Ile Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr 975 980 985 990		3099
cat gaa tta ggc cct ctg gta gat ttg aaa att cct gcc aac aag aca His Glu Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr 995 1000 1005		3147
cgg tgg act tta aaa aat tta aat ttc agc act cga tat aag ttt tat Arg Trp Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr 1010 1015 1020		3195
ttc tat gca caa aca tca gca gga tca gga agt caa att aca gag gaa Phe Tyr Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu 1025 1030 1035		3243
gca gta aca act gtg gat gaa gct ggt att ctt cca cct gat gta ggt Ala Val Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly 1040 1045 1050		3291
gca ggc aaa gtt caa gct gta aat acc agg atc agc aat ctt act gct Ala Gly Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala 1055 1060 1065 1070		3339
gca gct gct gag acc tat gcc aat atc agt tgg gaa tat gag gga cca Ala Ala Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro 1075 1080 1085		3387
gag cat gtg aac ttt tat gtt gaa tat ggt gta gca ggc agc aaa gaa Glu His Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu 1090 1095 1100		3435
gaa tgg aga aaa gaa att gta aat ggt tct cgg agc ttc ttt ggg tta Glu Trp Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu 1105 1110 1115		3483
aag ggt cta atg cca gga aca gca tac aaa gtt cga gtt ggt gct gtg Lys Gly Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val 1120 1125 1130		3531
ggg gac tct ggt ttt gtg agt tca gag gat gtg ttt gag aca ggc cca Gly Asp Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro 1135 1140 1145 1150		3579
gcg atg gca agc cgg cag gtg gat att gca act cag ggc tgg ttc att Ala Met Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile 1155 1160 1165		3627
ggt ctg atg tgt gct gtt ctc ctt atc tta att ttg ctg att gtt Gly Leu Met Cys Ala Val Ala Leu Leu Ile Leu Ile Leu Ile Val 1170 1175 1180		3675
tgc ttc atc aga aga aac aag ggt ggt aaa tat cca gtt aaa gaa aag		3723

20093A-21US-Substitute Sequence Listing.txt

Cys	Phe	Ile	Arg	Arg	Asn	Lys	Gly	Gly	Lys	Tyr	Pro	Val	Lys	Glu	Lys	
1185						1190					1195					
gaa	gat	gcc	cat	gct	gac	cct	gaa	atc	cag	cct	atg	aag	gaa	gat	gat	3771
Glu	Asp	Ala	His	Ala	Asp	Pro	Glu	Ile	Gln	Pro	Met	Lys	Glu	Asp	Asp	
1200				1205						1210						
ggg	aca	ttt	gga	gaa	tac	agt	gat	gca	gaa	gac	cac	aag	cct	ttg	aaa	3819
Gly	Thr	Phe	Gly	Glu	Tyr	Ser	Asp	Ala	Glu	Asp	His	Lys	Pro	Leu	Lys	
1215			1220					1225					1230			
aaa	gga	agt	cga	act	cct	tca	gac	agg	act	gtg	aaa	aaa	gaa	gat	agt	3867
Lys	Gly	Ser	Arg	Thr	Pro	Ser	Asp	Arg	Thr	Val	Lys	Lys	Glu	Asp	Ser	
1235					1240						1245					
gac	gac	agc	cta	gtt	gac	tat	gga	gaa	ggg	gtt	aat	ggc	cag	ttc	aat	3915
Asp	Asp	Ser	Leu	Val	Asp	Tyr	Gly	Glu	Gly	Val	Asn	Gly	Gln	Phe	Asn	
1250					1255						1260					
gag	gat	ggc	tcc	ttt	att	gga	caa	tac	agt	ggt	aag	aaa	gag	aaa	gag	3963
Glu	Asp	Gly	Ser	Phe	Ile	Gly	Gln	Tyr	Ser	Gly	Lys	Lys	Glu	Lys	Glu	
1265					1270					1275						
ccg	gct	gaa	gga	aac	gaa	agc	tca	gag	gca	cct	tct	cct	gtc	aac	gcc	4011
Pro	Ala	Glu	Gly	Asn	Glu	Ser	Ser	Glu	Ala	Pro	Ser	Pro	Val	Asn	Ala	
1280					1285					1290						
atg	aat	tcc	ttt	gtt	taa	tttttaagct	caaagccaat	attccatttc								4059
Met	Asn	Ser	Phe	Val												
1295					1300											
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Phe	Leu	Cys	Gln	Met	Ile	Ser	Ala	Leu	Glu	Val	Pro	Leu	Asp	Pro	Lys	
				20				25				30				
Leu	Leu	Glu	Asp	Leu	Val	Gln	Pro	Pro	Thr	Ile	Thr	Gln	Gln	Ser	Pro	
				35			40				45					
Lys	Asp	Tyr	Ile	Ile	Asp	Pro	Arg	Glu	Asn	Ile	Val	Ile	Gln	Cys	Glu	
				50			55				60					
Ala	Lys	Gly	Lys	Pro	Pro	Ser	Phe	Ser	Trp	Thr	Arg	Asn	Gly	Thr		
				65			70			75			80			
His	Phe	Asp	Ile	Asp	Lys	Asp	Pro	Leu	Val	Thr	Met	Lys	Pro	Gly	Thr	
				85				90					95			
Gly	Thr	Leu	Ile	Ile	Asn	Ile	Met	Ser	Glu	Gly	Lys	Ala	Glu	Thr	Tyr	
				100				105					110			
Glu	Gly	Val	Tyr	Gln	Cys	Thr	Ala	Arg	Asn	Glu	Arg	Gly	Ala	Ala	Val	
				115			120				125					
Ser	Asn	Asn	Ile	Val	Val	Arg	Pro	Ser	Arg	Ser	Pro	Leu	Trp	Thr	Lys	

20093A-21US-Substitute Sequence Listing.txt

130

135

140

Glu Lys Leu Glu Pro Ile Thr Leu Gln Ser Gly Gln Ser Leu Val Leu
 145 150 155 160

Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro Ile Ile Phe Trp Met
 165 170 175

Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu Arg Val Ser Gln Gly
 180 185 190

Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu Pro Glu Asp Thr Arg
 195 200 205

Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His Thr Gln Thr Ile Gln
 210 215 220

Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser Val Asp Glu Leu Asn
 225 230 235 240

Asp Thr Ile Ala Ala Asn Leu Ser Asp Thr Glu Phe Tyr Gly Ala Lys
 245 250 255

Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly Asn Ala
 260 265 270

Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu Cys Ile
 275 280 285

Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu Asp Gly
 290 295 300

Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys Thr Leu
 305 310 315 320

Gln Ile Ile His Val Ser Glu Ala Asp Ser Gly Asn Tyr Gln Cys Ile
 325 330 335

Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val Arg Val
 340 345 350

Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val Leu Ser
 355 360 365

Pro Gly Glu Asp Gly Thr Leu Ile Cys Arg Ala Asn Gly Asn Pro Lys
 370 375 380

Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile Ala Pro
 385 390 395 400

Asp Asp Pro Ser Arg Lys Ile Asp Gly Asp Thr Ile Ile Phe Ser Asn
 405 410 415

Val Gln Glu Arg Ser Ser Ala Val Tyr Gln Cys Asn Ala Ser Asn Glu
 420 425 430

Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala Glu Pro
 435 440 445

Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile Ala Asn
 450 455 460

Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu Pro Thr
 465 470 475 480

Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu Asp Ile
 485 490 495

20093A-21US-Substitute Sequence Listing.txt

Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Lys Asp Ala Thr Trp
500 505 510

Ile Val Lys Glu Ile Pro Val Ala Gln Lys Asp Ser Thr Gly Thr Tyr
515 520 525

Thr Cys Val Ala Arg Asn Lys Leu Gly Met Ala Lys Asn Glu Val His
530 535 540

Leu Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val Ser Phe
545 550 555 560

Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val Leu Trp
565 570 575

Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr Val Asp
580 585 590

Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser Gly Thr
595 600 605

Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala Ser Ala
610 615 620

Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val Tyr Asp
625 630 635 640

Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu Asp Lys
645 650 655

Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser Pro Ile
660 665 670

Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro Gly Leu
675 680 685

Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala Gln Leu
690 695 700

Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala Val Asn
705 710 715 720

Ser Ile Gly Lys Ser Leu Pro Ser Glu Ala Ser Glu Gln Tyr Leu Thr
725 730 735

Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly Leu Gly
740 745 750

Ser Glu Pro Asp Asn Leu Glu Ile Thr Trp Lys Pro Leu Asn Gly Phe
755 760 765

Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg Gln Lys
770 775 780

Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val Ser Lys
785 790 795 800

Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile Lys Val
805 810 815

Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val Val Met
820 825 830

Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn Val Arg
835 840 845

20093A-21US-Substitute Sequence Listing.txt

Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp Pro Val
 850 855 860
 Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile Tyr Tyr
 865 870 875 880
 Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile Glu Lys
 885 890 895
 Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu Pro Gly
 900 905 910
 Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val Asn Gly
 915 920 925
 Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr Pro Glu
 930 935 940
 Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro Thr Leu
 945 950 955 960
 Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn Gly Ile
 965 970 975
 Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr His Glu
 980 985 990
 Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr Arg Trp
 995 1000 1005
 Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr Phe Tyr
 1010 1015 1020
 Ala Gln Thr Ser Ala Gly Ser Gly Ser Gln Ile Thr Glu Glu Ala Val
 1025 1030 1035 1040
 Thr Thr Val Asp Glu Ala Gly Ile Leu Pro Pro Asp Val Gly Ala Gly
 1045 1050 1055
 Lys Val Gln Ala Val Asn Thr Arg Ile Ser Asn Leu Thr Ala Ala Ala
 1060 1065 1070
 Ala Glu Thr Tyr Ala Asn Ile Ser Trp Glu Tyr Glu Gly Pro Glu His
 1075 1080 1085
 Val Asn Phe Tyr Val Glu Tyr Gly Val Ala Gly Ser Lys Glu Glu Trp
 1090 1095 1100
 Arg Lys Glu Ile Val Asn Gly Ser Arg Ser Phe Phe Gly Leu Lys Gly
 105 1110 1115 1120
 Leu Met Pro Gly Thr Ala Tyr Lys Val Arg Val Gly Ala Val Gly Asp
 1125 1130 1135
 Ser Gly Phe Val Ser Ser Glu Asp Val Phe Glu Thr Gly Pro Ala Met
 1140 1145 1150
 Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly Trp Phe Ile Gly Leu
 1155 1160 1165
 Met Cys Ala Val Ala Leu Ile Leu Ile Leu Ile Val Cys Phe
 1170 1175 1180
 Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val Lys Glu Lys Glu Asp
 185 1190 1195 1200
 Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys Glu Asp Asp Gly Thr

20093A-21US-Substitute Sequence Listing.txt
1205 1210 1215

Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys Pro Leu Lys Lys Gly
1220 1225 1230

Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys Glu Asp Ser Asp Asp
1235 1240 1245

Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly Gln Phe Asn Glu Asp
1250 1255 1260

Gly Ser Phe Ile Gly Gln Tyr Ser Gly Lys Lys Glu Lys Glu Pro Ala
265 1270 1275 1280

Glu Gly Asn Glu Ser Ser Glu Ala Pro Ser Pro Val Asn Ala Met Asn
1285 1290 1295

Ser Phe Val

<210> 3
<211> 38
<212> DNA
<213> Homo sapiens

<400> 3
tctcatacta tgaacatatg ggttagaggt atattttc 38

<210> 4
<211> 123
<212> DNA
<213> Rattus norvegicus

<400> 4
tctcatacta tggacatatg ggttagaaaga atgtttctg cggtatatga gtattataag 60
aacagagcaa gaacataact cagtcagtca gatgatacgt taatatgaac tgggtgaaa 120
agg 123

<210> 5
<211> 176
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: clone D4-1

<400> 5
tctcatacta tgaacatatg ggttagaggt atatttctg ctgtatgtta gtattatgag 60
aatagttaca gcaaaaacat aactcagtca aagtataatgt taatatgaac tggaatgcaa 120
aagtgcatac ttttcattc aaaatggta ttcttgattt cctaaaaaaa aaaaaa 176

<210> 6
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 6

20093A-21US-Substitute Sequence Listing.txt
tagataacaac tagtcaatgc ctctaatgaa tatggata 38

<210> 7
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 7
agatagatcc gcggaatagt aaatccgata gccttgta 38

<210> 8
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> CDS
<222> (1)
<223> n=a, c, g, or t

<400> 8
ngctgctctc atact 15

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 9
aacatatggg tagagagtat attt 24

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
ctttgcattc cagttcatat taa 23

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 11
tgtggtgaca gatcacggct 20

20093A-21US-Substitute Sequence Listing.txt

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 12
cagctcaaac ctgtgatttc c 21

<210> 13
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
aataggtatt ggtgaattta aagactcaact ctccataaaat gctacgaata tttaaacactt 60

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
cgagcaata tgaaatgatc t 21

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
gcaatacag ctcctattg 19

<210> 16
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
gctgtatgtt agtattatga gaatagttac agcaaaaaca taa 43

<210> 17
<211> 40
<212> DNA
<213> Artificial Sequence

<220>

20093A-21US-Substitute Sequence Listing.txt

<223> Description of Artificial Sequence: primer

<400> 17
taggcctgac tggcattgt a ttagcaaact catcaactaga 40

<210> 18
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
tagatacaac tagtcta atg cagcttaaaa taatgcc 37

<210> 19
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
agatagatcc gcggatatcc atattcatta gaggcattg 39

<210> 20
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
tagatacaac tagtcaatgc ctctaatgaa tatggata 38

<210> 21
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
agatagatcc gcgaaatagt aaatccgata gccttgta 38

<210> 22
<211> 61
<212> DNA
<213> Homo sapiens

<220>
<223> Description of Artificial Sequence: primer

<400> 22
aggagttaag atgcta atgc agcttaaaa atgccc gaaa aagaagcgct tatctgc ggg 60

c 61

20093A-21US-Substitute Sequence Listing.txt

<210> 23
<211> 19
<212> DNA
<213> Homo sapiens

<400> 23
cattagcatc ttaactcct 19

<210> 24
<211> 21
<212> DNA
<213> Homo sapiens

<400> 24
tcggcattat tttaagctgc a 21

<210> 25
<211> 17
<212> DNA
<213> Homo sapiens

<400> 25
gcagataagc gcttctt 17

<210> 26
<211> 20
<212> DNA
<213> Homo sapiens

<400> 26
actagagata cagatcatat 20

<210> 27
<211> 20
<212> DNA
<213> Homo sapiens

<400> 27
catatacgat cgatcgatgc 20

<210> 28
<211> 20
<212> DNA
<213> Homo sapiens

<400> 28
gatagtgcgt atcgatgcta 20

<210> 29
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 29
catacgaatt ctagatacaa ctagtctaat gcagcttaaa ataatgcc 48

20093A-21US-Substitute Sequence Listing.txt

<210> 30

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 30

agatagatcc gcggatatcc atattcatta gaggcattgg gatccatac

50

<210> 31

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 31

atgccaaaaa agaagcgctt atctgcgggc agagtgc(ccc tgattcttt cctgtgccag 60

atgatttagtg cactggaagt acctcttgat ccaaaaacttc ttgaagactt ggtacagcct 120

ccaaaccatca cccaaacagtc tccaaaagat tacattattt accctcgggga gaatatttta 180

atccagtgta aagccaaagg gaaaccgccc ccaagctttt cctggaccgg taatggact 240

cattttgaca tcgataaaaga ccctctggtc accatgaagc ctggcacagg aacgctata 300

attaacatca tgagcgaagg gaaagctgag acctatgaag gagtctatca gtgtacagca 360

aggaacgaac gcggagctgc agtttctaattt aacatttttg tccgcccattt cagatcacca 420

tttgtggacca aagaaaaact tgaaccaatc acacttcaaa gtggtcagtc ttttagtactt 480

ccctgcagac ccccaatttg attaccacca cctataatat tttggatgga taattccctt 540

caaagacttc cacaaagtga gagagttctt caaggttga atggggaccc ttattttcc 600

aatgtcctcc cagaggacac ccgcgaagac tatatctgtt atgctagatt taatcatact 660

caaaccatac agcagaagca acctatttctt gtgaagggtga tttcagtggta tgaattgaat 720

gacactatag ctgctaattt gagtgacact gagttttagt gtgctaaatc aagtagagag 780

aggccaccaa catttttaac tccagaaggc aatgcaagta acaaagagga attaagagga 840

aatgtgcttt cactggagtg cattgcagaa ggactgccta ccccaatttat ttactggca 900

aaggaagatg gaatgctacc caaaaacagg acagtttata agaactttga gaaaacctt 960

cagatcattt atgtttcaga agcagactctt ggaaatttacc aatgtatagc aaaaaatgca 1020

tttaggagcca tccaccatac catttctgtt agagttaaag cggctccata ctggatcaca 1080

gccccctcaaa atcttgcgt gtccccagga gaggatggga ccttgcattt cagagctaat 1140

ggcaacccca aacccagaat tagctggta acaaatggag tcccaataga aattgcccct 1200

gatgacccca gcagaaaaat agatggcgat accattttt tttcaaattgt tcaagaaaga 1260

tcaagtgcag tatatcagtg caatgcctctt aatgaatatg gatatttact ggcaaacgca 1320

tttggtaatg tgctggctga gccaccacga atcctcacac ctgcaaacac a 1371

<210> 32

<211> 1371

20093A-21US-Substitute Sequence Listing.txt

<212> DNA

<213> Rattus norvegicus

<400> 32

atgccagaaga agaagccctt gtctgcaggc agagcgc(ccc tgtttctctt cctgtgccag 60
atgatcagcg ctctggatgt tcctcttgat ccaaagctcc ttgatgactt ggtacagcct 120
ccaactatca ctcAACAGTC accaaaagac tacatcattg acccacggga gaatattgta 180
atccaatgtg aggccaaagg gaaacctcct ccaagctttt cctggactcg taacggaaca 240
catttgaca tagacaaaga ccctctggtc actatgaagc ctggctcagg aacccttgc 300
atcaacatca tgagtgaagg aaaggcggag acctatgaag gggtttacca gtgcactgca 360
aggaatgagc gcggagctgc tgtctccaat aacattgtt tccgcccctc taggtcaccc 420
ttgtggacca aggaaagact tgaaccaata atcctccgaa gtggtcagtc actagtacta 480
ccatgttaggc ctccaattgg attaccacccg gccataatat tttggatgga taactcctt 540
caaagactgc cacagagtga gcgggttcc caaggactga atggagaccc ttacttctcc 600
aatgtcctcc cagaggacac ccgtgaggac tacatctgct atgccagatt taatcacact 660
caaacaattc aacagaaaca acctatttct ctgaaggtga tttcagtgga tgaattgaat 720
gacactatag ctgctaattt gagtgacact gagttttagt gtgctaaatc tagtaaagag 780
aggccaccaa catttctaac tccagagggc aatgaaagtc acaaggaaga attaagagga 840
aacgtgcttt ccctggagtg cattgcagaa ggcctaccta ctccagttat ttactggatc 900
aaggaagatg gaacgcttcc tgtcaaccgg acgttttac ggaactttaa gaaaaccttg 960
cagatcattc atgtctctga agcagactct ggaaatttac agtgcatacg aaaaaacgc 1020
ttgggagccg tccatcatac catttctgtc acagttaaag cggctcccta ctggattgtt 1080
gcacccatcaca acctcgtgct ttccccaggg gagaatggga ccctcatctg cagagctaac 1140
ggcaacccaa aacccagaat tagctggta acaaatggag tcccagtaga aattgctctc 1200
gatgacccca gccaaaaat cgatggtgat accattatgt tttcaaatgt tcaagaaagc 1260
tcaagtgcgg tttatcagtg caatgcctct aacaaatatg gatatttact agcaaatgca 1320
tttgtaaatg tgctcgctga accacctcg accacacctt cagcaaacac a 1371

<210> 33

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: pLXSN MCS (EcoRI and
BamHI cloning site)

<400> 33

gcgccggaaat tcgttaacct cgaggatccg gctgtg

36